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Gln Gln Tyr Asn Ile Tyr Pro Leu Thr
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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn				
20	25	30		
gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa ctc ctc atc				144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile				
35	40	45		
tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga				192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly				
50	55	60		
tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca				240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro				
65	70	75	80	
gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc				288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu				
85	90	95		
aca ttc ggt cag ggt act aaa gta gaa atc aaa				321
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys				
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Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile			
35	40	45	
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly			
50	55	60	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro			
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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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tcc gtc aaa gtt tct tgt aag gcc tca ggc tac gtg ttc aca gac tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30
ggt atg aat tgg gtc aga cag gcc ccg gga caa ggc ctg gaa tgg atg 144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
ggt tgg att aat act tac att gga gag cct att tat gct caa aag ttc 192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
50 55 60
cag ggc aga gtc acg ttc act cta gac acc tcc aca agc act gca tac 240
Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
atg gag ctg tca tct ctg aga tcc gag gac acc gca gtg tac tat tgt 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110
cta gtc aca gtc tcc tca 354
Leu Val Thr Val Ser Ser
115

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1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 14
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Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<400> 16
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<210> 17
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<220>

<223> Primer CH4

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<223> Primer CH5

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<223> Primer CH6

<400> 22

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<210> 23

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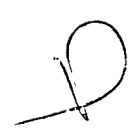
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Gly Val Pro Tyr Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Thr Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys
20 25 30

<210> 93
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework L4

<400> 93

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1 5 10

<210> 94
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework L4



<400> 94

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
1 5 10

<210> 95

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework H1

<400> 95

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 96

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework H1

<400> 96

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr
20 25 30

<210> 97

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework H2

<400> 97

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10



<210> 98
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H2

<400> 98

Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met Gly
1 5 10

<210> 99
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework H3

<400> 99

Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 100
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H3

<400> 100

Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe Leu Gln
1 5 10 15

Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
20 25 30

<210> 101
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework H4



<400> 101

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 102

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework H4

<400> 102

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 103

<211> 324

<212> DNA

<213> Murine

<220>

<221> CDS

<222> (1)..(324)

<223>

<400> 103

gac att gtg atg acc cag tct caa aaa ttc atg tcc aca tca gta gga 48
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

gta gcc tgg tat caa cag aaa cca gga caa tct cct aaa gca ctg att 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

tac tcg gca tcc ttc cta tat agt gga gtc cct tat cgc ttc aca ggc 192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly
50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc act gtg cag tct 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser
65 70 75 80

gaa gac ttg gca gag tat ttc tgt cag caa tat aac atc tat cct ctc 288
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

D

acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgt
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 100 105

324

<210> 104
 <211> 108
 <212> PRT
 <213> Murine

<400> 104

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser
 65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 100 105

<210> 105
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hTNF40 heavy chain variable domain

<220>
 <221> CDS
 <222> (1) .. (354)
 <223>

<400> 105
 cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu

48



1	5	10	15	
aca gtc aag atc tcc tgc aag gct tct gga tat gtt ttc	aca gac tat	96		
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr				
20	25	30		
gga atg aat tgg gtg aag cag gct cca gga aag gct ttc aag tgg atg		144		
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met				
35	40	45		
ggc tgg ata aac acc tac att gga gag cca ata tat gtt gat gac ttc		192		
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe				
50	55	60		
aag gga cga ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt		240		
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe				
65	70	75	80	
ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt		288		
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys				
85	90	95		
gca aga ggt tac cgg tcc tat gct atg gac tac tgg ggt caa gga acc		336		
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr				
100	105	110		
tca gtc acc gtc tct tca		354		
Ser Val Thr Val Ser Ser				
115				

<210> 106
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hTNF40 heavy chain variable domain

<400> 106

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu	
1 5 10 15	
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr	
20 25 30	
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met	
35 40 45	
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe	
50 55 60	



Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 107
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> OmpA oligonucleotide adaptor

<220>
<221> CDS
<222> (29)..(67)
<223>

<400> 107
tcgagttcta gataacgagg cgtaaaaa atg aaa aag aca gct atc gca att 52
Met Lys Lys Thr Ala Ile Ala Ile
1 5

gca gtg gcc ttg gct ctgacgtacg agtcagg 84
Ala Val Ala Leu Ala
10

<210> 108
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> OmpA oligonucleotide adaptor

<400> 108

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala
1 5 10

<210> 109
<211> 67
<212> DNA

2

<213> Artificial Sequence

<220>

<223> IGS cassette-1

<220>

<221> CDS

<222> (2) .. (40)

<223>

<220>

<221> CDS

<222> (43) .. (66)

<223>

<400> 109

g	agc	tca	cca	gta	aca	aaa	agt	ttt	aat	aga	gga	gag	tgt	ta	atg	aag	48
	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		Met	Lys	
1					5					10						15	

aag	act	gct	ata	gca	att	g	67
Lys	Thr	Ala	Ile	Ala	Ile		
					20		

<210> 110

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-1

<400> 110

Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys
1				5					10			

<210> 111

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-1

<400> 111

Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile
1				5			

<210> 112

<211> 69



<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<220>
<221> CDS
<222> (2)..(43)
<223>

<220>
<221> CDS
<222> (45)..(68)
<223>

<400> 112
g agc tca cca gta aca aaa agt ttt aat aga ggg gag tgt taa a atg 47
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Met
1 5 10

aag aag act gct ata gca att g 69
Lys Lys Thr Ala Ile Ala Ile
15 20

<210> 113
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<400> 113

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10


<210> 114
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<400> 114

Met Lys Lys Thr Ala Ile Ala Ile
1 5

<210> 115



<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<220>
<221> CDS
<222> (2)..(43)
<223>

<220>
<221> CDS
<222> (57)..(80)
<223>

<400> 115
g agc tca cca gta aca aaa agc ttt aat aga gga gag tgt tga 43
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

ggaggaaaaa aaa atg aag aaa act gct ata gca att g 81
Met Lys Lys Thr Ala Ile Ala Ile
15 20

<210> 116
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<400> 116

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

<210> 117
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<400> 117

Met Lys Lys Thr Ala Ile Ala Ile
1 5

B

<210> 118
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<220>
<221> CDS
<222> (2)..(43)
<223>

<220>
<221> CDS
<222> (57)..(80)
<223>

<400> 118
g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt tga 43
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

cgaggattat ata atg aag aaa act gct ata gca att g 81
Met Lys Lys Thr Ala Ile Ala Ile
15 20

<210> 119
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<400> 119
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

<210> 120
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<400> 120
Met Lys Lys Thr Ala Ile Ala Ile
1 5

D

<210> 121
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 3 consensus framework H1

<400> 121

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

<210> 122
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 3 consensus framework H2

<400> 122

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 123
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 3 consensus framework H3

<400> 123

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 124
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

D

<223> Human group 3 consensus framework H4

<400> 124

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 125

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for fab

<400> 125

gaggttcagc tggtcgagtc aggaggcggc ctcgtgcagc ctggcggatc actgagattg 60
tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120
ccgggaaagg gcctggaatg gatggggttg attaatactt acattggaga gcctatttat 180
gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240
ctccaaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300
agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctcagcttcc 360
accaagggcc catcgggtctt ccccttgga cctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggc caaggactac ttccccgaac cggtgacggc gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagtt 648

<210> 126

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for fab

<400> 126

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30

D

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val
210 215

<210> 127

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted light chain for fab and modified fab

D

<400> 127
gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60
atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca 120
ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180
aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca 240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300
ggtactaaag tagaaatcaa acgtacggta ggggccccat ctgtcttcat cttcccgcga 360
tctgatgagc agttgaaatc tggaactgcc tctgttggtg gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccacaggggc 600
ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 128
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Grafted light chain for fab and modified fab

<400> 128

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

D

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 129
 <211> 687
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Grafted heavy chain for modified fab

<400> 129
 gaggttcagc tggctcgagtc aggaggcggc ctcgtgcagc ctggcggatc actgagattg 60
 tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120
 ccgggaaagg gcctggaatg gatggggttgg attaatactt acattggaga gcctatttat 180
 gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240
 ctccaaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300
 agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctcagcttcc 360
 accaagggcc catcgggtctt cccctggga cctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggc caaggactac ttccccgaac cggtgacggc gtcgtggaac 480

D

145

150

155

160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Ala Ala
225

D